

M. Dali

1646

## RAW SEQUENCE LISTING

DATE: 05/04/2000

PATENT APPLICATION: US/09/199,874B

TIME: 06:18:47

Input Set : A:\Sequence

Output Set: N:\CRF3\05042000\I199874B.raw

4 <110> APPLICANT: Segre, Gino V.  
 5 Kronenberg, Henry M.  
 6 Abou-Samra, Abdul-Badi  
 7 Juppner, Harald  
 8 Potts, Jr., John T.  
 9 Schipani, Ernestina  
 11 <120> TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME  
 13 <130> FILE REFERENCE: 00786/071005  
 15 <140> CURRENT APPLICATION NUMBER: US 09/199,874B  
 16 <141> CURRENT FILING DATE: 1998-11-24  
 18 <150> PRIOR APPLICATION NUMBER: US 08/471,494  
 19 <151> PRIOR FILING DATE: 1995-06-06  
 21 <160> NUMBER OF SEQ ID NOS: 21  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1862  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Didelphoidea  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (98)...(1642)  
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 36 gtggccccgt tggactcggc cctagggaac ggcggcg atg gga gcg ccc cgg atc 115  
 37 Met Gly Ala Pro Arg Ile  
 38 1 5  
 40 tgc cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc 163  
 41 Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val  
 42 10 15 20  
 44 tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc 211  
 45 Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile  
 46 25 30 35  
 48 att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag 259  
 49 Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu  
 50 40 45 50  
 52 gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca 307  
 53 Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser  
 54 55 60 65 70  
 56 agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc 355  
 57 Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro  
 58 75 80 85  
 60 cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat 403  
 61 Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp  
 62 90 95 100  
 64 ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga 451  
 65 Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly  
 66 105 110 115

ENTERED

TC 1000 MAIL ROOM

RECEIVED

MAY 26 2000

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68	gtg	ccc	ggc	aag	gtg	gtg	gcc	gtg	ccc	tgc	ccc	gac	tac	ttc	tac	gac	499
69	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
70		120					125					130					
72	ttc	aac	cac	aaa	ggc	cga	gcc	tat	cgg	cgc	tgt	gac	agc	aat	ggc	agc	547
73	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
74	135					140					145				150		
76	tgg	gag	ctg	gtg	cct	ggg	aac	aac	cgg	aca	tgg	gcg	aat	tac	agc	gaa	595
77	Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
78					155				160					165			
80	tgt	gtc	aag	ttt	ctg	acc	aac	gag	acc	cgg	gaa	cgg	gaa	gtc	ttt	gat	643
81	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
82			170					175					180				
84	cgc	ctc	gga	atg	atc	tac	act	gtg	ggc	tac	tcc	atc	tct	ctg	ggc	tcc	691
85	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
86		185					190					195					
88	ctc	act	gtg	gct	gtg	ctg	att	ctg	ggt	tac	ttt	agg	agg	tta	cat	tgc	739
89	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
90		200				205				210							
92	acc	cga	aac	tac	att	cac	atg	cat	ctc	ttc	gtg	tcc	ttt	atg	ctc	cgg	787
93	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
94	215				220					225				230			
96	gct	gta	agc	atc	ttc	atc	aag	gat	gct	gtg	ctc	tac	tcg	ggg	gtt	tcc	835
97	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
98			235					240				245					
100	aca	gat	gaa	atc	gag	cgc	atc	acc	gag	gag	gag	ctg	agg	gcc	ttc	aca	883
101	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
102			250					255				260					
104	gag	cct	ccc	cct	gct	gac	aag	gcg	ggt	ttt	gtg	ggc	tgc	aga	gtg	gcg	931
105	Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
106			265				270					275					
108	gta	acc	gtc	ttc	ctt	tac	ttc	ctg	acc	acc	aac	tac	tac	tgg	atc	ctg	979
109	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
110		280				285					290						
112	gtg	gaa	ggc	ctc	tac	ctt	cac	agc	ctc	atc	ttc	atg	gct	ttt	ttc	tct	1027
113	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	
114	295				300					305				310			
116	gag	aaa	aag	tat	ctc	tgg	ggt	ttc	aca	tta	ttt	ggc	tgg	ggc	ctc	cct	1075
117	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
118				315				320				325					
120	gcc	gtg	ttt	gtc	gct	gtg	tgg	gtg	acc	gtg	agg	gct	aca	ctg	gcc	aac	1123
121	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
122			330				335					340					
124	act	gag	tgc	tgg	gac	ctg	agt	tcg	ggg	aat	aag	aaa	tgg	atc	ata	cag	1171
125	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
126		345				350					355						
128	gtg	ccc	atc	ctg	gca	gct	att	gtg	gtg	aac	ttt	att	ctt	ttt	atc	aat	1219
129	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
130		360				365				370							
132	ata	atc	aga	gtc	ctg	gct	act	aaa	ctc	cgg	gag	acc	aat	gca	ggg	aga	1267

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133 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
134 375 380 385 390
136 tgt gac acg agg caa cag tat aga aag ctg ctg aag tcc acg cta gtc 1315
137 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Lys Ser Thr Leu Val
138 395 400 405
140 ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg 1363
141 Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro
142 410 415 420
144 tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa 1411
145 Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu
146 425 430 435
148 atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt 1459
149 Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys
150 440 445 450
152 ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga 1507
153 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg
154 455 460 465 470
156 tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt 1555
157 Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser
158 475 480 485
160 acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg 1603
161 Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val
162 490 495 500
164 gga cct cga ggg ggc tgg cct tgt ccc tca gcc ctc gac tagctcctgg 1652
165 Gly Pro Arg Gly Gly Trp Pro Cys Pro Ser Ala Leu Asp
166 505 510 515
168 ggctggagcc agtgcgaatg gccatcacca gttgcctggc tatgtgaagc atgggtccat 1712
169 ttctgagaac tcattgcctt catctggccc agagcctggc accaaagatg acgggtatct 1772
170 caatggctct ggactttatg agccaatggt tggggaacag cccctccac tcctggagga 1832
171 ggagagagag acagtcattg gacccatatt 1862
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 1863
175 <212> TYPE: DNA
176 <213> ORGANISM: Didelphoidea
178 <220> FEATURE:
179 <221> NAME/KEY: CDS
180 <222> LOCATION: (98)...(1852)
182 <400> SEQUENCE: 2
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184 gtggccccgt tggactcggc ctagggaac ggcggcg atg gga gcg ccc cgg atc 115
185 Met Gly Ala Pro Arg Ile
186 1 5
188 tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc 163
189 Ser His Ser Leu Ala Leu Leu Cys Cys Ser Val Leu Ser Ser Val
190 10 15 20
192 tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc 211
193 Tyr Ala Leu Val Asp Ala Asp Val Ile Thr Lys Glu Glu Gln Ile
194 25 30 35
196 att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag 259

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197	Ile	Leu	Leu	Arg	Asn	Ala	Gln	Ala	Gln	Cys	Glu	Gln	Arg	Leu	Lys	Glu	
198		40				45					50						
200	gtc	ctc	agg	gtc	cct	gaa	ctt	gct	gaa	tct	gcc	aaa	gac	tgg	atg	tca	307
201	Val	Leu	Arg	Val	Pro	Glu	Leu	Ala	Glu	Ser	Ala	Lys	Asp	Trp	Met	Ser	
202	55					60					65				70		
204	agg	tct	gca	aag	aca	aag	aag	gag	aaa	cct	gca	gaa	aag	ctt	tat	ccc	355
205	Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	
206					75					80					85		
208	cag	gca	gag	gag	tcc	agg	gaa	gtt	tct	gac	agg	agc	cgg	ctg	cag	gat	403
209	Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	
210					90				95					100			
212	ggc	ttc	tgc	cta	cct	gag	tgg	gac	aac	att	gtg	tgc	tgg	cct	gct	gga	451
213	Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Ala	Gly	
214			105				110						115				
216	gtg	ccc	ggc	aag	gtg	gtg	gcc	gtg	ccc	tgc	ccc	gac	tac	ttc	tac	gac	499
217	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	
218		120				125						130					
220	ttc	aac	cac	aaa	ggc	cga	gcc	tat	cgg	cgc	tgt	gac	agc	aat	ggc	agc	547
221	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser	
222	135					140					145				150		
224	tgg	gag	ctg	gtg	cct	ggg	aac	aac	cgg	aca	tgg	gcg	aat	tac	agc	gaa	595
225	Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	
226					155					160					165		
228	tgt	gtc	aag	ttt	ctg	acc	aac	gag	acc	cgg	gaa	cgg	gaa	gtc	ttt	gat	643
229	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	
230				170					175					180			
232	cgc	ctc	gga	atg	atc	tac	act	gtg	ggc	tac	tcc	atc	tct	ctg	ggc	tcc	691
233	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser	
234			185					190					195				
236	ctc	act	gtg	gct	gtg	ctg	att	ctg	ggg	tac	ttt	agg	agg	tta	cat	tgc	739
237	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys	
238		200				205						210					
240	acc	cga	aac	tac	att	cac	atg	cat	ctc	ttc	gtg	tcc	ttt	atg	ctc	cgg	787
241	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	
242	215					220					225				230		
244	gct	gta	agc	atc	ttc	atc	aag	gat	gct	gtg	ctc	tac	tcg	ggg	gtt	tcc	835
245	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser	
246					235					240				245			
248	aca	gat	gaa	atc	gag	cgc	atc	acc	gag	gag	gag	ctg	agg	gcc	ttc	aca	883
249	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
250				250					255					260			
252	gag	cct	ccc	cct	gct	gac	aag	gcg	ggg	ttt	gtg	ggc	tgc	aga	gtg	gcg	931
253	Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
254			265					270					275				
256	gta	acc	gtc	ttc	ctt	tac	ttc	ctg	acc	acc	aac	tac	tac	tgg	atc	ctg	979
257	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
258		280				285						290					
260	gtg	gaa	ggc	ctc	tac	ctt	cac	agc	ctc	atc	ttc	atg	gct	ttt	ttc	tct	1027
261	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	

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262 295          300          305          310
264 gag aaa aag tat ctc tgg ggt ttc aca tta ttt ggc tgg ggc ctc cct      1075
265 Glu Lys Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro
266          315          320          325
268 gcc gtg ttt gtc gct gtg tgg gtg acc gtg agg gct aca ctg gcc aac      1123
269 Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn
270          330          335          340
272 act gag tgc tgg gac ctg agt tgc ggg aat aag aaa tgg atc ata cag      1171
273 Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln
274          345          350          355
276 gtg ccc atc ctg gca gct att gtg gtg aac ttt att ctt ttt atc aat      1219
277 Val Pro Ile Leu Ala Ala Ile Val Val Asn Phe Ile Leu Phe Ile Asn
278          360          365          370
280 ata atc aga gtc ctg gct act aaa ctc cgg gag acc aat gca ggg aga      1267
281 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg
282          375          380          385          390
284 tgt gac acg agg caa cag tat aga aag ctg ctg aag tcc acg cta gtc      1315
285 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val
286          395          400          405
288 ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg      1363
289 Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro
290          410          415          420
292 tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa      1411
293 Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu
294          425          430          435
296 atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt      1459
297 Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys
298          440          445          450
300 ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga      1507
301 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg
302          455          460          465          470
304 tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt      1555
305 Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser
306          475          480          485
308 acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg      1603
309 Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val
310          490          495          500
312 gga cct cga ggg ggg ctg gcc ttg tcc ctc agc cct cga cta gct cct      1651
313 Gly Pro Arg Gly Gly Leu Ala Asn Gly His His Gln Leu Pro Gly Tyr Val
314          505          510          515
316 ggg gct gga gcc agt gcc aat ggc cat cac cag ttg cct ggc tat gtg      1699
317 Gly Ala Gly Ala Ser Ala Asn Gly His His Gln Leu Pro Gly Tyr Val
318          520          525          530
320 aag cat ggt tcc att tct gag aac tca ttg cct tca tct ggc cca gag      1747
321 Lys His Gly Ser Ile Ser Glu Asn Ser Leu Pro Ser Ser Gly Pro Glu
322          535          540          545          550
324 cct ggc acc aaa gat gac ggg tat ctc aat ggc tct gga ctt tat gag      1795
325 Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn Gly Ser Gly Leu Tyr Glu
326          555          560          565

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 05/04/2000

PATENT APPLICATION: US/09/199,874B

TIME: 06:18:48

Input Set : A:\Sequence

Output Set: N:\CRF3\05042000\I199874B.raw

L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8